



1600

RAW SEQUENCE LISTING

DATE: 08/08/2002

PATENT APPLICATION: US/09/498,556B

TIME: 11:01:41

Input Set : A:\Corvas Seq. Listing.txt

Output Set: N:\CRF4\08082002\I498556B.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Corvas International , Inc.
 4 Vlasuk, George Phillip
 5 Stanssens, Patrick Eric Hugo
 6 Messens, Joris Hila Lieven
 7 Lauwereys, Marc Josef
 8 Laroche, Yves Rene
 9 Jespers, Laurent Stephane
 10 Gansemans, Yannick Georges Jozef
 11 Moyle, Matthew
 12 Bergum, Peter W.
 14 <120> TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND
 ANTICOAGULANT PROTEIN
 16 <130> FILE REFERENCE: 018813/0272487
 18 <140> CURRENT APPLICATION NUMBER: 09/498,556B
 19 <141> CURRENT FILING DATE: 2000-04-02
 21 <150> PRIOR APPLICATION NUMBER: 08/809,455
 22 <151> PRIOR FILING DATE: 1997-04-17
 24 <150> PRIOR APPLICATION NUMBER: PCT/US95/13231
 25 <151> PRIOR FILING DATE: 1995-10-17
 27 <150> PRIOR APPLICATION NUMBER: 08/486,399
 28 <151> PRIOR FILING DATE: 1995-06-05
 30 <150> PRIOR APPLICATION NUMBER: 08/486,397
 31 <151> PRIOR FILING DATE: 1995-06-05
 33 <150> PRIOR APPLICATION NUMBER: 08/465,380
 34 <151> PRIOR FILING DATE: 1995-06-05
 36 <150> PRIOR APPLICATION NUMBER: 08/461,965
 37 <151> PRIOR FILING DATE: 1995-06-05
 39 <150> PRIOR APPLICATION NUMBER: 08/326,110
 40 <151> PRIOR FILING DATE: 1994-10-18
 42 <160> NUMBER OF SEQ ID NOS: 357
 44 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

233 <210> SEQ ID NO: 8
 234 <211> LENGTH: 79
 235 <212> TYPE: PRT
 236 <213> ORGANISM: Ascylostoma caninum
 238 <400> SEQUENCE: 8
 240 Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu
 241 1 5 10 15
 242 Asp Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu Glu
 243 20 25 30

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244 Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro Gly Pro Ala
 245 35 40 45
 246 Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp
 247 50 55 60
 E--> 248 Cys Val Lys Glu Glu Glu Cys Asp Gln His Glu Ile Ile His Val
 249 65 70 75
 1269 <210> SEQ ID NO: 36
 1270 <211> LENGTH: 686
 1271 <212> TYPE: DNA
 1272 <213> ORGANISM: Ancylostoma caninum
 1274 <220> FEATURE:
 1275 <221> NAME/KEY: CDS
 1276 <222> LOCATION: (14)..(556)
 1278 <220> FEATURE:
 1279 <221> NAME/KEY: misc_feature
 1280 <223> OTHER INFORMATION: Recombinant cDNA Molecule AcaNAP45
 1282 <400> SEQUENCE: 36
 1284 aattccgga aaa atg ctg atg ctc tac ctt gtt cct atc tgg ttg cta 48
 1285 Met Leu Met Leu Tyr Leu Val Pro Ile Trp Leu Leu
 1286 1 5 10
 E--> 1287 ctc att tcg caa tgc agt gga aaa tcc gcg aag aaa tgt ggt ctc aat (98) 96
 1288 Leu Ile Ser Gln Cys Ser Gly Lys Ser Ala Lys Lys Cys Gly Leu Asn
 1289 15 20 25
 E--> 1290 gaa aaa ttg gac tgt ggc aat ctg aag gca tgc gag aaa aag tgc agc (146) 144
 1291 Glu Lys Leu Asp Cys Gly Asn Leu Lys Ala Cys Glu Lys Lys Cys Ser
 1292 30 35 40
 E--> 1293 gac ttg gac aat gag gag gat tat aag gag gaa gat gag tcg aaa tgc 194
 1294 Asp Leu Asp Asn Glu Glu Asp Tyr Lys Glu Glu Asp Glu Ser Lys Cys
 1295 45 50 55 60
 E--> 1296 cga tca cgt gaa tgt agt cgt cgt gtt tgt gta tgc gat gaa gga ttc 242
 1297 Arg Ser Arg Glu Cys Ser Arg Arg Val Cys Val Cys Asp Glu Gly Phe
 1298 65 70 75
 E--> 1299 tac aga aac aag aag ggc caa tgt gtg aca aga gat gat tgc gag tat 290
 1300 Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg Asp Asp Cys Glu Tyr
 1301 80 85 90
 E--> 1302 gac aat atg gag att atc act ttt cca cca gaa gat aaa tgt ggt ccc 338
 1303 Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Lys Cys Gly Pro
 1304 95 100 105
 E--> 1305 gat gaa tgg ttc gac tgg tgt gga act tac aag cag tgt gag cgc aag 386
 1306 Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys Gln Cys Glu Arg Lys
 1307 110 115 120
 E--> 1308 tgc aat aag gag cta agt gag aaa gat gaa gag gca tgc ctc tca cgt 434
 1309 Cys Asn Lys Glu Leu Ser Glu Lys Asp Glu Glu Ala Cys Leu Ser Arg
 1310 125 130 135 140
 E--> 1311 gct tgt act ggt cgt gct tgt gtt tgc aac gac gga ctg tac aga gac 482
 1312 Ala Cys Thr Gly Arg Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp
 1313 145 150 155
 E--> 1314 gat ttt ggc aat tgt gtt gag aaa gac gaa tgt aac gat atg gag att 530
 1315 Asp Phe Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu Ile

Invalid
amino acid
designator

Val ← use lower-case
letters for
amino acid

nos.
off

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Input Set : A:\Corvas Seq. Listing.txt

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```

1316          160          165          170
E--> 1317 atc act ttt cca ccg gaa acc aaa cac tgaccaaagg ctctaactct cgctacat 585
1318 Ile Thr Phe Pro Pro Glu Thr Lys His
1319          175          180
E--> 1320 aacgtcagtg cttgaattgc cccittacga gtttagtaatt ttgactaact ctgtgtaatt 645
E--> 1322 gagcattgtc tactgatggg gaaaatgaag tgttcaatgt ct 686
1526 <210> SEQ ID NO: 42
1527 <211> LENGTH: 74
1528 <212> TYPE: PRT
1529 <213> ORGANISM: Ancylostoma caninum
1531 <220> FEATURE:
1532 <221> NAME/KEY: misc_feature
1533 <223> OTHER INFORMATION: Alignment of amino acid sequences to mature AcaNAP48
1535 <400> SEQUENCE: 42
1537 Arg Thr Ala Arg Lys Pro Pro Thr Cys Gly Glu Asn Glu Arg Val Glu
1538 1          5          10          15
1539 Trp Cys Gly Lys Gln Cys Glu Ile Thr Cys Asp Asp Pro Asp Lys Ile
1540          20          25          30
1541 Cys Arg Ser Leu Ala Cys Pro Gly Pro Pro Ala Cys Val Cys Asp Asp
E--> 1542 35          40          45
1543 Gly Tyr Tyr Arg Asp Thr Asn Val Gly Leu Cys Val Gln Tyr Asp Glu
E--> 1544 50          55          60
1545 Cys Asn Asp Met Asp Ile Ile Met Val Ser
E--> 1546 65          70
1816 <210> SEQ ID NO: 52
1817 <211> LENGTH: 83
1818 <212> TYPE: PRT
1819 <213> ORGANISM: Ancylostoma duodenale
1821 <220> FEATURE:
1822 <221> NAME/KEY: misc_feature
1823 <223> OTHER INFORMATION: Alignment of amino acid sequences to mature
1824 AduNAP7d1 and AduNAP4d1
1826 <400> SEQUENCE: 52
1828 Lys Ala Ala Lys Lys Cys Gly Leu Asn Glu Arg Leu Asp Cys Gly Asn
E--> 1829 1          5          10          15
1830 Leu Lys Gln Cys Glu Pro Lys Cys Ser Asp Leu Glu Ser Glu Glu Tyr
1831          20          25          30
1832 Glu Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser Arg Arg
1833          35          40          45
1834 Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Lys Cys
E--> 1835 50          55          60
1836 Val Ala Lys Asp Val Cys Glu Asp Asp Asn Met Glu Ile Ile Thr Phe
E--> 1837 65          70          75          80
1838 Pro Pro Glu
2105 <210> SEQ ID NO: 62
2106 <211> LENGTH: 171
2107 <212> TYPE: PRT
2108 <213> ORGANISM: Ancylostoma ceylanicum
2110 <400> SEQUENCE: 62

```

has.
off
↓

misaligned
amino acid

nos. - see

item 3

in Enn

summary

sheet

misaligned
amino acid
nos.

p.4

RAW SEQUENCE LISTING

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Input Set : A:\Corvas Seq. Listing.txt

Output Set: N:\CRF4\08082002\I498556B.raw

2112 Lys Pro Asn Asn Val Met Thr Asn Ala Cys Gly Leu Asn Glu Tyr Phe
2113 1 5 10 15
2114 Ala Glu Cys Gly Asn Met Lys Glu Cys Glu His Arg Cys Asn Glu Glu
2115 20 25 30
2116 Glu Asn Glu Glu Arg Asp Glu Glu Arg Ile Thr Ala Cys Leu Ile Arg
2117 35 40 45
2118 Val Cys Phe Arg Pro Gly Ala Cys Val Cys Lys Asp Gly Phe Tyr Arg
2119 50 55 60
2120 Asn Arg Thr Gly Ser Cys Val Glu Glu Asp Asp Cys Glu Tyr Glu Asn
2121 65 70 75 80
2122 Met Glu Phe Ile Thr Phe Ala Pro Glu Val Pro Ile Cys Gly Ser Asn
2123 85 90 95
2124 Glu Arg Tyr Ser Asp Cys Gly Asn Asp Lys Gln Cys Glu Arg Lys Cys
2125 100 105 110
2126 Asn Glu Asp Asp Tyr Glu Lys Gly Asp Glu Ala Cys Arg Ser His Val
E--> 2127 115 120 125
2128 Cys Glu Arg Pro Gly Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asn
E--> 2129 130 135 140
2130 Lys Lys Gly Ser Cys Val Glu Ser Asp Asp Cys Glu Tyr Asp Asn Met
E--> 2131 145 150 155 160
2132 Asp Phe Ile Thr Phe Ala Pro Glu Thr Ser Arg
E--> 2133 165 170
2202 <210> SEQ ID NO: 65
2203 <211> LENGTH: 161
2204 <212> TYPE: PRT
2205 <213> ORGANISM: Ancylostoma duodenale
2207 <400> SEQUENCE: 65
2209 Lys Ala Ala Lys Lys Cys Gly Leu Asn Glu Arg Leu Asp Cys Gly Asn
2210 1 5 10 15
2211 Leu Lys Gln Cys Glu Pro Lys Cys Ser Asp Leu Glu Ser Glu Glu Tyr
2212 20 25 30
2213 Glu Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser Arg Arg
E--> 2214 35 40 45
2215 Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys Lys Gly Lys Cys
E--> 2216 50 55 60
2217 Val Ala Lys Asp Val Cys Glu Asp Asp Asn Met Glu Ile Ile Thr Phe
E--> 2218 65 70 75 80
2219 Pro Pro Glu Asp Glu Cys Gly Pro Asp Glu Trp Phe Asp Tyr Cys Gly
E--> 2220 85 90 95
2222 Asn Tyr Lys Lys Cys Glu Arg Lys Cys Ser Glu Glu Thr Ser Glu Lys
E--> 2223 100 105 110
2224 Asn Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val
E--> 2225 115 120 125
2226 Cys Lys Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Pro His
E--> 2227 130 135 140
2228 Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys
E--> 2229 145 150 155 160
2230 His
2324 <210> SEQ ID NO: 72

*misaligned**nos.**misaligned**nos.**PS*

RAW SEQUENCE LISTING
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Input Set : A:\Corvas Seq. Listing.txt
Output Set: N:\CRF4\08082002\I498556B.raw

2326 <211> LENGTH: 5
2327 <212> TYPE: PRT
2328 <213> ORGANISM: Ancylostoma caninum
2330 <400> SEQUENCE: 72
E--> 2332 Gly Try Tyr Arg Asn
2333 1 5 *invalid*
2706 <210> SEQ ID NO: 97
2707 <211> LENGTH: 20
2708 <212> TYPE: PRT
2709 <213> ORGANISM: Ancylostoma caninum
2711 <220> FEATURE:
2712 <221> NAME/KEY: misc_feature
2713 <223> OTHER INFORMATION: N-terminal fragment
2715 <400> SEQUENCE: 97
E--> 2717 Gys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Tip Leu Asp Asp Cys Gly Thr
2718 1 5 10 15 *invalid*
2719 Gln Lys Pro
2720 20
3184 <210> SEQ ID NO: 127
3185 <211> LENGTH: 46
3186 <212> TYPE: DNA
3187 <213> ORGANISM: Ancylostoma caninum
3189 <220> FEATURE:
3190 <221> NAME/KEY: misc_feature
3191 <223> OTHER INFORMATION: Oligonucleotide primer
3193 <400> SEQUENCE: 127
E--> 3195 cgctctagaa gcttcattggg ttctgagttc cggtatat aaagtc 46 *invalid*
3198 <210> SEQ ID NO: 128
3199 <211> LENGTH: 91
3200 <212> TYPE: PRT
3201 <213> ORGANISM: Ancylostoma caninum
3203 <220> FEATURE:
3204 <221> NAME/KEY: misc_feature
3205 <223> OTHER INFORMATION: Alignment of AcaNAPc2
3207 <400> SEQUENCE: 128
E--> 3209 Leu Val Sar Tyr Cys Ser Gly Lys Ala Thr Met Gln Cys Gly Glu Asn
3210 1 5 10 15
3213 Glu Lys Tyr Asp Ser Cys Gly Ser Lys Glu Cys Asp Lys Lys Cys Lys
3214 20 25 30
3215 Tyr Asp Gly Val Glu Glu Glu Asp Asp Glu Glu Pro Asn Val Pro Cys
3216 35 40 45
3217 Leu Val Arg Val Cys His Gln Asp Cys Val Cys Glu Glu Gly Phe Tyr
3218 50 55 60
3219 Arg Asn Lys Asp Asp Lys Cys Val Ser Ala Glu Asp Cys Glu Leu Asp
3220 65 70 75 80
3221 Asn Met Asp Phe Ile Tyr Pro Gly Thr Arg Asn
3222 85 90
3329 <210> SEQ ID NO: 135
3330 <211> LENGTH: 20

*invalid for use in
the sequence
instead,
use
Xaa
and
Hydro
in <220>-<223>
section*

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Input Set : A:\Corvas Seq. Listing.txt

Output Set: N:\CRF4\08082002\I498556B.raw

3331 <212> TYPE: PRT
 3332 <213> ORGANISM: Ancylostoma caninum
 3334 <220> FEATURE:
 W--> 3335 <221> NAME/KEY: Internal fragment
 3336 <223> OTHER INFORMATION: Xaa in locations 1 to 3 and 5 to 20 is any amino acid
 3338 <400> SEQUENCE: 135
 W--> 3340 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 E--> 3341 1 5 10 15 *misaligned nos.*
 W--> 3342 Xaa Xaa Xaa Xaa
 3343 20
 5239 <210> SEQ ID NO: 236
 5240 <211> LENGTH: 23
 5241 <212> TYPE: PRT
 5242 <213> ORGANISM: Ancylostoma caninum
 5244 <220> FEATURE:
 W--> 5245 <221> NAME/KEY: Internal fragment
 5246 <223> OTHER INFORMATION: Xaa in location 2 to 23 is any amino acid
 5248 <400> SEQUENCE: 236
 W--> 5250 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 5251 1 5 10 15
 W--> 5252 Xaa Xaa Xaa Xaa Xaa Xaa Xaa *misaligned nos.*
 E--> 5253 20
 5256 <210> SEQ ID NO: 237
 5257 <211> LENGTH: 22
 5258 <212> TYPE: PRT
 5259 <213> ORGANISM: Ancylostoma caninum
 5261 <220> FEATURE:
 W--> 5262 <221> NAME/KEY: Internal fragment
 5263 <223> OTHER INFORMATION: Xaa in location 2 to 22 is any amino acid
 W--> 5264 <400> SEQUENCE: 237
 W--> 5266 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 E--> 5267 1 5 10 15
 W--> 5268 Xaa Xaa Xaa Xaa Xaa Xaa *misaligned nos.*
 E--> 5269 20
 5279 <210> SEQ ID NO: 238
 5280 <211> LENGTH: 21
 5281 <212> TYPE: PRT
 5282 <213> ORGANISM: Ancylostoma caninum
 5284 <220> FEATURE:
 W--> 5285 <221> NAME/KEY: Internal fragment
 5286 <223> OTHER INFORMATION: Xaa in location 2 to 21 is any amino acid
 5288 <400> SEQUENCE: 238
 W--> 5290 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 E--> 5291 1 5 10 15
 W--> 5292 Xaa Xaa Xaa Xaa Xaa *misaligned nos.*
 E--> 5293 20
 5296 <210> SEQ ID NO: 239
 5297 <211> LENGTH: 20
 5298 <212> TYPE: PRT

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Input Set : A:\Corvas Seq. Listing.txt

Output Set: N:\CRF4\08082002\I498556B.raw

5299 <213> ORGANISM: Ancylostoma caninum
5301 <220> FEATURE:
W--> 5302 <221> NAME/KEY: Internal fragment
5303 <223> OTHER INFORMATION: Xaa in location 2 to 20 is any amino acid
5305 <400> SEQUENCE: 239
W--> 5307 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5308 1 5 10 15
W--> 5309 Xaa Xaa Xaa Xaa
E--> 5310 20 *misaligned nos.*
5313 <210> SEQ ID NO: 240
5314 <211> LENGTH: 19
5315 <212> TYPE: PRT
5316 <213> ORGANISM: Ancylostoma caninum
5318 <220> FEATURE:
W--> 5319 <221> NAME/KEY: Internal fragment
5320 <223> OTHER INFORMATION: Xaa in location 2 to 19 is any amino acid
5322 <400> SEQUENCE: 240
W--> 5324 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5325 1 5 10 15
W--> 5326 Xaa Xaa Xaa *misaligned nos.*
5336 <210> SEQ ID NO: 241
5337 <211> LENGTH: 18
5338 <212> TYPE: PRT
5339 <213> ORGANISM: Ancylostoma caninum
5341 <220> FEATURE:
W--> 5342 <221> NAME/KEY: Internal fragment
5343 <223> OTHER INFORMATION: Xaa in location 2 to 18 is any amino acid
5345 <400> SEQUENCE: 241
W--> 5347 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5348 1 5 10 15
W--> 5349 Xaa Xaa *misaligned nos.*
5352 <210> SEQ ID NO: 242
5353 <211> LENGTH: 17
5354 <212> TYPE: PRT
5355 <213> ORGANISM: Ancylostoma caninum
5357 <220> FEATURE:
W--> 5358 <221> NAME/KEY: Internal fragment
5359 <223> OTHER INFORMATION: Xaa in location 2 to 17 is any amino acid
5361 <400> SEQUENCE: 242
W--> 5363 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5364 1 5 10 15
W--> 5365 Xaa *misaligned nos.*
5368 <210> SEQ ID NO: 243
5369 <211> LENGTH: 16
5370 <212> TYPE: PRT
5371 <213> ORGANISM: Ancylostoma caninum
5373 <220> FEATURE:
W--> 5374 <221> NAME/KEY: Internal fragment
5375 <223> OTHER INFORMATION: Xaa in location 2 to 16 is any amino acid

RAW SEQUENCE LISTING

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Input Set : A:\Corvas Seq. Listing.txt

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5377 <400> SEQUENCE: 243
W--> 5379 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5380 1 5 10 15 *misaligned seq.*
5393 <210> SEQ ID NO: 244
5394 <211> LENGTH: 15
5395 <212> TYPE: PRT
5396 <213> ORGANISM: Ancylostoma caninum
5398 <220> FEATURE:
W--> 5399 <221> NAME/KEY: Internal fragment
5400 <223> OTHER INFORMATION: Xaa in locations 2 to 15 is any amino acid
5402 <400> SEQUENCE: 244
W--> 5404 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5405 1 5 10 15 *misaligned seq.*
5408 <210> SEQ ID NO: 245
5409 <211> LENGTH: 14
5410 <212> TYPE: PRT
5411 <213> ORGANISM: Ancylostoma caninum
5413 <220> FEATURE:
W--> 5414 <221> NAME/KEY: Internal fragment
5415 <223> OTHER INFORMATION: Xaa in locations 2 to 14 is any amino acid
5417 <400> SEQUENCE: 245
W--> 5419 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5420 1 5 10 *misaligned seq.*
5423 <210> SEQ ID NO: 246
5424 <211> LENGTH: 13
5425 <212> TYPE: PRT
5426 <213> ORGANISM: Ancylostoma caninum
5428 <220> FEATURE:
W--> 5429 <221> NAME/KEY: Internal fragment
5430 <223> OTHER INFORMATION: Xaa in locations 2 to 13 is any amino acid
5432 <400> SEQUENCE: 246
W--> 5434 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5435 1 5 10 *misaligned seq.*
5452 <210> SEQ ID NO: 247
5453 <211> LENGTH: 12
5454 <212> TYPE: PRT
5455 <213> ORGANISM: Ancylostoma caninum
5457 <220> FEATURE:
W--> 5458 <221> NAME/KEY: Internal fragment
5459 <223> OTHER INFORMATION: Xaa in locations 2 to 12 is any amino acid
5461 <400> SEQUENCE: 247
W--> 5463 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 5464 1 5 10 *misaligned seq.*
5469 <210> SEQ ID NO: 248
5470 <211> LENGTH: 11
5471 <212> TYPE: PRT
5472 <213> ORGANISM: Ancylostoma caninum
5474 <220> FEATURE:
W--> 5475 <221> NAME/KEY: Internal fragment

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Input Set : A:\Corvas Seq. Listing.txt

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5476 <223> OTHER INFORMATION: Xaa in locations 2 to 11 is any amino acid
 5478 <400> SEQUENCE: 248
 W--> 5480 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 E--> 5481 1 5 10 *misaligned*
 5484 <210> SEQ ID NO: 249
 5485 <211> LENGTH: 10
 5486 <212> TYPE: PRT
 5487 <213> ORGANISM: Ancylostoma caninum
 5489 <220> FEATURE:
 W--> 5490 <221> NAME/KEY: Internal fragment
 5491 <223> OTHER INFORMATION: Xaa in locations 2 to 10 is any amino acid
 5493 <400> SEQUENCE: 249
 W--> 5495 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 E--> 5496 1 5 10 *misaligned*
 5513 <210> SEQ ID NO: 250
 5514 <211> LENGTH: 9
 5515 <212> TYPE: PRT
 5516 <213> ORGANISM: Ancylostoma caninum
 5518 <220> FEATURE:
 W--> 5519 <221> NAME/KEY: Internal fragment
 5520 <223> OTHER INFORMATION: Xaa in locations 2 to 9 is any amino acid
 5522 <400> SEQUENCE: 250
 W--> 5524 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 E--> 5525 1 5 *misaligned*

↓
 The errors shown exist throughout
 the sequence Listing. Please check subsequent
 sequences for similar errors.

See following pages for more errors

<210> 3
 <211> 461
 <212> DNA
 <213> Ancylostoma caninum

<220>
 <221> CDS
 <222> (22)..(321)

<220>
 <221> misc_feature
 <223> AcaNAPs cDNA sequence

<400> 3

```

gaattccgct actactcaac a atg aag atg ctt tac gct atc gct ata atg      51
                        Met Lys Met Leu Tyr Ala Ile Ala Ile Met
                        1           5           10
ttt ctc ctg gta tca tta tgc agc gca aga aca gtg agg aag gca tac      99
Phe Leu Leu Val Ser Leu Cys Ser Ala Arg Thr Val Arg Lys Ala Tyr
                        15           20           25
cgc gag tgt ggt gag aat gaa tgg ctc gac gac tgt gga act cag aag    147
Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Asp Cys Gly Thr Gln Lys
                        30           35           40
cca tgc gag gcc aag tgc aat gag gaa ccc cct gag gag gaa gat ccg    195
Pro Cys Glu Ala Lys Cys Asn Glu Glu Pro Pro Glu Glu Glu Asp Pro
                        45           50           55
ata tgc cgc tca cgt ggt tgt tta tta cct cct gct tgc gta tgc aaa    243
Ile Cys Arg Ser Arg Gly Cys Leu Leu Pro Pro Ala Cys Val Cys Lys
                        60           65           70
    
```

Sample of misaligned amino acid nos.
in a coding sequence. Please ensure
all coding sequences show properly
aligned amino acid nos.

<210> 116

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Description of Artificial Sequence: pUC119 primer

misspelled - should be Artificial

*(please correct all misspellings
of this word)*

09/498, 556B 12

<210> 118

<211> 7

<212> PRT

<213> *mandatory response needed*

<220>

<221> misc_feature

<223> Xaa in location 5 is Arg, Pro or Lys

<400> 118

Lys Pro Cys Glu Xaa Lys Cys

1

5

09/498, 556B 13

<210> 176
<211> 6
<212> PRT
<213> Ancylostoma caninum

<220> Internal fragment

<221> Xaa in locations 2 to 6 is any amino acid

<400> 176

Cys Xaa Xaa Xaa Xaa Xaa
1 5

never insert a response to <220>. It is a
"header" only.

(Same error in
Sequence 314)

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/498,556B

DATE: 08/08/2002
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Input Set : A:\Corvas Seq. Listing.txt
Output Set: N:\CRF4\08082002\I498556B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:68; Line(s) 2279
Seq#:78; Line(s) 2401
Seq#:79; Line(s) 2416
Seq#:80; Line(s) 2434
Seq#:81; Line(s) 2448
Seq#:82; Line(s) 2463
Seq#:84; Line(s) 2503
Seq#:91; Line(s) 2614
Seq#:111; Line(s) 2914
Seq#:112; Line(s) 2940
Seq#:113; Line(s) 2954
Seq#:114; Line(s) 2968
Seq#:115; Line(s) 2994
Seq#:119; Line(s) 3050

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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:66; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:67; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:68; Xaa Pos. 1,2,3,4,5,6,7
Seq#:78; Xaa Pos. 1,2
Seq#:79; Xaa Pos. 1,2
Seq#:80; Xaa Pos. 1,2
Seq#:81; Xaa Pos. 1,2
Seq#:82; Xaa Pos. 1,2
Seq#:83; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:84; Xaa Pos. 1,2,3,4
Seq#:85; Xaa Pos. 1,2,3,4
Seq#:86; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:87; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:90; N Pos. 6
Seq#:91; N Pos. 6,9,18
Seq#:94; N Pos. 6,12,21
Seq#:118; Xaa Pos. 5
Seq#:119; Xaa Pos. 2,4,5,7
Seq#:129; Xaa Pos. 2,3,4,5,6,7,8
Seq#:130; Xaa Pos. 2,3,4,5,6
Seq#:131; Xaa Pos. 2,3,4,5
Seq#:132; Xaa Pos. 2,3,4
Seq#:133; Xaa Pos. 2,3
Seq#:134; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21
Seq#:135; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20
Seq#:136; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:137; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18
Seq#:138; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:139; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:140; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15
Seq#:141; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14
Seq#:142; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13
Seq#:143; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12
Seq#:144; Xaa Pos. 1,2,3,5,6,7,8,9,10,11
Seq#:145; Xaa Pos. 1,2,3,5,6,7,8,9,10
Seq#:146; Xaa Pos. 2,3,4,5
Seq#:147; Xaa Pos. 2,3,4
Seq#:148; Xaa Pos. 2,3,4,5,6
Seq#:149; Xaa Pos. 2,3,4,5
Seq#:150; Xaa Pos. 2,3,4
Seq#:151; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:152; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14
Seq#:153; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13

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Seq#:154; Xaa Pos. 2,3,4,5,6,7
Seq#:155; Xaa Pos. 2,3,4,5,6
Seq#:156; Xaa Pos. 2,3,4,5,6,7,8
Seq#:157; Xaa Pos. 2,3,4,5,6
Seq#:158; Xaa Pos. 2,3,4,5
Seq#:159; Xaa Pos. 2,3,4
Seq#:160; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:160; Xaa Pos. 23
Seq#:161; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:162; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21
Seq#:163; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20
Seq#:164; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:165; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18
Seq#:166; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:167; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:168; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15
Seq#:169; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14
Seq#:170; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13
Seq#:171; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12
Seq#:172; Xaa Pos. 1,2,3,5,6,7,8,9,10,11
Seq#:173; Xaa Pos. 1,2,3,5,6,7,8,9,10
Seq#:174; Xaa Pos. 2,3,4,5
Seq#:175; Xaa Pos. 2,3,4
Seq#:176; Xaa Pos. 2,3,4,5,6
Seq#:177; Xaa Pos. 2,3,4,5
Seq#:178; Xaa Pos. 2,3,4
Seq#:179; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:180; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14
Seq#:181; Xaa Pos. 2,3,4,5,6,7,8
Seq#:182; Xaa Pos. 2,3,4,5,6,7
Seq#:183; Xaa Pos. 2,3,4,5,6
Seq#:184; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:184; Xaa Pos. 23,24,25,26
Seq#:185; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:185; Xaa Pos. 23,24,25
Seq#:186; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:186; Xaa Pos. 23,24
Seq#:187; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:187; Xaa Pos. 23
Seq#:188; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:189; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21
Seq#:190; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20
Seq#:191; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:192; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18
Seq#:193; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:194; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:195; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:196; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14
Seq#:197; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13

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Seq#:198; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12
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Seq#:202; Xaa Pos. 2,3,4,5,6,7,8
Seq#:203; Xaa Pos. 2,3,4,5,6,7
Seq#:204; Xaa Pos. 2,3,4,5,6
Seq#:205; Xaa Pos. 2,3,4,5,6,7,8
Seq#:206; Xaa Pos. 2,3,4,5,6
Seq#:207; Xaa Pos. 2,3,4,5
Seq#:208; Xaa Pos. 2,3,4
Seq#:209; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:209; Xaa Pos. 23
Seq#:210; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:211; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21
Seq#:212; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20
Seq#:213; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:214; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18
Seq#:215; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:216; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:217; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15
Seq#:218; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14
Seq#:219; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13
Seq#:220; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12
Seq#:221; Xaa Pos. 1,2,3,5,6,7,8,9,10,11
Seq#:222; Xaa Pos. 1,2,3,5,6,7,8,9,10
Seq#:223; Xaa Pos. 2,3,4,5
Seq#:224; Xaa Pos. 2,3,4
Seq#:225; Xaa Pos. 2,3,4,5,6
Seq#:226; Xaa Pos. 2,3,4,5
Seq#:227; Xaa Pos. 2,3,4
Seq#:228; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:229; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14
Seq#:230; Xaa Pos. 2,3,4,5,6,7,8
Seq#:231; Xaa Pos. 2,3,4,5,6,7
Seq#:232; Xaa Pos. 2,3,4,5,6
Seq#:233; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:233; Xaa Pos. 23,24,25,26
Seq#:234; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:234; Xaa Pos. 23,24,25
Seq#:235; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:235; Xaa Pos. 23,24
Seq#:236; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:236; Xaa Pos. 25
Seq#:237; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:238; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23
Seq#:239; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22
Seq#:240; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:241; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18

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Seq#:242; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:243; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:244; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:245; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14
Seq#:246; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13
Seq#:247; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12
Seq#:248; Xaa Pos. 2,3,4,5,6,7,8,9,10,11
Seq#:249; Xaa Pos. 2,3,4,5,6,7,8,9,10
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Seq#:251; Xaa Pos. 2,3,4,5,6,7,8
Seq#:252; Xaa Pos. 2,3,4,5,6,7
Seq#:253; Xaa Pos. 2,3,4,5,6
Seq#:254; Xaa Pos. 2,3,4,5,6,7,8
Seq#:255; Xaa Pos. 2,3,4,5,6
Seq#:256; Xaa Pos. 2,3,4,5
Seq#:257; Xaa Pos. 2,3,4
Seq#:258; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:258; Xaa Pos. 25
Seq#:259; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:260; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23
Seq#:261; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20
Seq#:262; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:263; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18
Seq#:264; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:265; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:266; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15
Seq#:267; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14
Seq#:268; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13
Seq#:269; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12
Seq#:270; Xaa Pos. 1,2,3,5,6,7,8,9,10,11
Seq#:271; Xaa Pos. 1,2,3,5,6,7,8,9,10
Seq#:272; Xaa Pos. 2,3,4,5
Seq#:273; Xaa Pos. 2,3,4
Seq#:274; Xaa Pos. 2,3,4,5,6
Seq#:275; Xaa Pos. 2,3,4,5
Seq#:276; Xaa Pos. 2,3,4
Seq#:277; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:278; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14
Seq#:279; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13
Seq#:280; Xaa Pos. 2,3,4,5,6,7,8
Seq#:281; Xaa Pos. 2,3,4,5,6,7
Seq#:282; Xaa Pos. 2,3,4,5,6
Seq#:283; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:283; Xaa Pos. 25,26,27,28
Seq#:284; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:284; Xaa Pos. 25,26,27
Seq#:285; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:285; Xaa Pos. 25,26
Seq#:286; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24

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Seq#:286; Xaa Pos. 25
Seq#:287; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:288; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,20,21,22,23,24
Seq#:289; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22
Seq#:290; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:291; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18
Seq#:292; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:293; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:294; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:295; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14
Seq#:296; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13
Seq#:297; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12
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Seq#:299; Xaa Pos. 2,3,4,5,6,7,8,9,10
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Seq#:301; Xaa Pos. 2,3,4,5,6,7,8
Seq#:302; Xaa Pos. 2,3,4,5,6,7
Seq#:303; Xaa Pos. 2,3,4,5,6
Seq#:304; Xaa Pos. 2,3,4,5
Seq#:305; Xaa Pos. 2,3,4
Seq#:306; Xaa Pos. 2,3
Seq#:307; Xaa Pos. 2
Seq#:308; Xaa Pos. 2,3,4,5,6,7,8
Seq#:309; Xaa Pos. 2,3,4,5,6
Seq#:310; Xaa Pos. 2,3,4,5
Seq#:311; Xaa Pos. 2,3,4
Seq#:312; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:312; Xaa Pos. 25
Seq#:313; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:314; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23
Seq#:315; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22
Seq#:316; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:317; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18
Seq#:318; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:319; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:320; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15
Seq#:321; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14
Seq#:322; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13
Seq#:323; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12
Seq#:324; Xaa Pos. 1,2,3,5,6,7,8,9,10,11
Seq#:325; Xaa Pos. 1,2,3,5,6,7,8,9,10
Seq#:326; Xaa Pos. 2,3,4,5
Seq#:327; Xaa Pos. 2,3,4
Seq#:328; Xaa Pos. 2,3,4,5,6
Seq#:329; Xaa Pos. 2,3,4,5
Seq#:330; Xaa Pos. 2,3,4
Seq#:331; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:332; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13,14
Seq#:333; Xaa Pos. 2,3,4,5,6,7,8

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Seq#:334; Xaa Pos. 2,3,4,5,6,7
Seq#:335; Xaa Pos. 2,3,4,5,6
Seq#:336; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:336; Xaa Pos. 25,26,27,28
Seq#:337; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:337; Xaa Pos. 25,26,27
Seq#:338; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:338; Xaa Pos. 25,26
Seq#:339; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:339; Xaa Pos. 25
Seq#:340; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23,24
Seq#:341; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22,23
Seq#:342; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,19,20,21,22
Seq#:343; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
Seq#:344; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18
Seq#:345; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
Seq#:346; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16
Seq#:347; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15
Seq#:348; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14
Seq#:349; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13
Seq#:350; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12
Seq#:351; Xaa Pos. 2,3,4,5,6,7,8,9,10,11
Seq#:352; Xaa Pos. 2,3,4,5,6,7,8,9,10
Seq#:353; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:354; Xaa Pos. 2,3,4,5,6,7,8
Seq#:355; Xaa Pos. 2,3,4,5,6,7
Seq#:356; Xaa Pos. 2,3,4,5,6
Seq#:357; Xaa Pos. 2,4

VERIFICATION SUMMARY

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Input Set : A:\Corvas Seq. Listing.txt

Output Set: N:\CRF4\08082002\I498556B.raw

L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:101 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:248 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:341 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:369 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:381 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:525 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:528 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:531 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:697 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:700 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:719 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:1125 M:112 C: (48) String data converted to lower case,
L:1287 M:254 E: No. of Bases conflict, LENGTH:Input:98 Counted:96 SEQ:36
M:254 Repeated in SeqNo=36
L:1322 M:252 E: No. of Seq. differs, <211> LENGTH:Input:686 Found:685 SEQ:36
L:1542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
M:332 Repeated in SeqNo=42
L:1829 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:52
M:332 Repeated in SeqNo=52
L:2127 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:62
M:332 Repeated in SeqNo=62
L:2214 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:65
M:332 Repeated in SeqNo=65
L:2244 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66
L:2244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0
L:2268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:67
L:2268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0
L:2283 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:68
L:2283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0
L:2332 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:2405 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:78

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L:2405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:0
L:2420 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:79
L:2420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
L:2437 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:80
L:2437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:0
L:2452 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:81
L:2452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
L:2467 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:82
L:2467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
L:2492 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:83
L:2492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
L:2507 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:84
L:2507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
L:2522 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:85
L:2522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0
L:2547 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:86
L:2547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
L:2562 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:87
L:2562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
L:2582 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:89
L:2604 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90
L:2604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90 after pos.:0
L:2618 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:2618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
L:2675 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:94
L:2675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:94 after pos.:0
L:2717 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:2
L:3004 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:116
L:3028 M:201 W: Mandatory field data missing, <213> ORGANISM
L:3036 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:118
L:3036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118 after pos.:0
L:3054 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:119
L:3054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:119 after pos.:0
L:3195 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:3209 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:3231 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:129
L:3236 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:129
L:3236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129 after pos.:0
L:3248 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:130
L:3253 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:130
L:3253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130 after pos.:0
L:3263 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:131
L:3268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:131
L:3268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:0
L:3278 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:132
L:3283 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:132
L:3283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132 after pos.:0
L:3293 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:133
L:3298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:133

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L:3298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:0
L:3308 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:134
L:3313 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:134
L:3313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134 after pos.:0
L:3315 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:134
L:3315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134 after pos.:16
L:3335 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:135
L:3340 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:135
L:3340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:0
L:3341 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:135
L:3342 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:135
L:3342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:16
L:3352 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:136
L:3357 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:136
L:3357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136 after pos.:0
L:3359 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:136
L:3359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136 after pos.:16
L:3368 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:137
L:3373 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:137
L:3373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:0
L:3375 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:137
L:3375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:16
L:3384 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:138
L:3389 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:138
L:3389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0
L:3391 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:138
L:3391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:16
L:3400 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:139
L:3405 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:139
L:3405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:3415 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:140
L:3420 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:140
L:3420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:3430 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:141
L:3435 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:141
L:3435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:3449 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:142
L:3454 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:142
L:3454 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:3464 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:143
L:3469 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:143
L:3469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:0
L:3479 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:144
L:3484 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:144
L:3484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144 after pos.:0
L:3506 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:145
L:3511 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:145
L:3511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145 after pos.:0
L:3521 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:146

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L:3526 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:146
L:3526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:0
L:3536 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:147
L:3541 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:147
L:3541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:147 after pos.:0
L:3563 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:148
L:3568 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:148
L:3568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:148 after pos.:0
L:3578 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:149
L:3583 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:149
L:3583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:149 after pos.:0
L:3593 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:150
L:3598 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:150
L:3598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:150 after pos.:0
L:3620 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:151
L:3625 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:151
L:3625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:151 after pos.:0
L:3635 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:152
L:3640 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:152
L:3640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152 after pos.:0
L:3650 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:153
L:3655 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:153
L:3655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:153 after pos.:0
L:3677 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:154
L:3682 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:154
L:3682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:154 after pos.:0
L:3692 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:155
L:3697 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:155
L:3697 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:155 after pos.:0
L:3707 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:156
L:3734 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:157
L:3749 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:158
L:3764 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:159
L:3793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:160
L:3810 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:161
L:3827 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:162
L:3850 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:163
L:3867 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:164
L:3884 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:165
L:3908 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:166
L:3924 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:167
L:3939 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:168
L:3966 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:169
L:3981 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:170
L:3996 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:171
L:4023 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:172
L:4038 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:173
L:4055 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:174
L:4082 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:175

VERIFICATION SUMMARY

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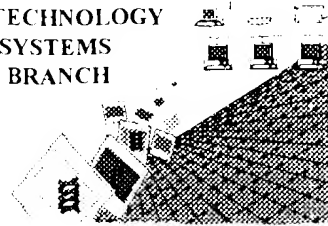
TIME: 11:01:43

Input Set : A:\Corvas Seq. Listing.txt

Output Set: N:\CRF4\08082002\I498556B.raw

L:4096 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:5253 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:236
L:5264 M:283 W: Missing Blank Line separator, <400> field identifier
L:5267 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:237
M:332 Repeated in SeqNo=237
L:5291 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:238
M:332 Repeated in SeqNo=238
L:5308 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:239
M:332 Repeated in SeqNo=239
L:5325 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:240
L:5348 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:241
L:5364 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:242
L:5380 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:243
L:5405 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:244
L:5420 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:245
L:5435 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:246
L:5464 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:247
L:5481 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:248
L:5496 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:249
L:5525 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:250
L:5540 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:251
L:5555 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:252
L:5582 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:253
L:5598 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:254
L:5613 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:255
L:5641 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:256
L:5656 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:257
L:5671 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:258
M:332 Repeated in SeqNo=258
L:5698 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:259
M:332 Repeated in SeqNo=259
L:5715 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:260
M:332 Repeated in SeqNo=260
L:5732 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:261
L:5755 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:262
L:5771 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:263
L:5787 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:264
L:5812 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:265
L:5827 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:266
L:5842 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:267
L:5869 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:268
L:5884 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:269
L:5900 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:270
L:6746 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:7187 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/498,556B
Source: 1600
Date Processed by STIC: 8/7/2002

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/498,556B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

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